

# Assessment of the genetic diversity of wild kuruma prawn based on the relatedness analysis using microsatellites DNA and mitochondrial DNA markers

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# Annual catches of kuruma prawn have been unstable in Japan



# Huge amounts of the prawns have been released around Japan

15 - 20 millions/year

Japan Sea

50 millions/year

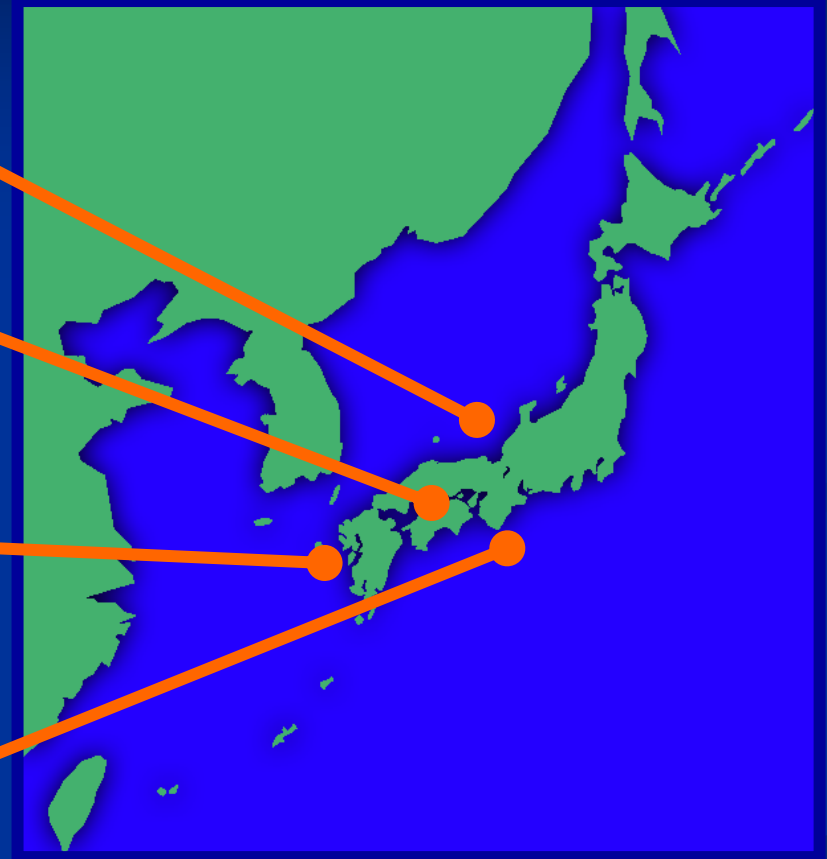
Seto Inland Sea

40 millions/year

East China Sea

35 - 40 millions/year

Pacific Ocean



...However, cost and benefit of the stocking are still ambiguous.

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## *1. Assessment of genetic diversity of the wild population*

- Population genetic analyses based on allele frequency
- Population genetic analyses based on relatedness

## *2. Assessment of genetic diversity of stocked population*

- Population genetic analyses based on relatedness

# Sampling locations of kuruma prawn



# The DNA markers used in this study

## *Microsatellites DNA (MS-DNA) marker*

Loci	Repeat motif
<i>CSPJ002*</i>	(GA) <sub>n</sub>
<i>CSPJ010*</i>	(GAA) <sub>n</sub> GCA(GAA) <sub>m</sub>
<i>CSPJ012*</i>	(CTT) <sub>n</sub> CCT(CTT) <sub>m</sub> CAT(CTT) <sub>1</sub>
<i>CSPJ014*</i>	GAAAAA(GAA) <sub>n</sub> GAAAAA
<i>CSPJ015*</i>	(CTT) <sub>n</sub>

## *Mitochondrial DNA (mtDNA) PCR-RFLP marker*



# The heterogeneities of prawns in Kumamoto and Kagoshima were suggested by HWE test

Loci	Aichi	Ehime	Kuma- moto	Kago- shima
<i>CSPJ002*</i>	—	—	+	+
<i>CSPJ010*</i>	+	—	+	+
<i>CSPJ012*</i>	—	—	—	+
<i>CSPJ014*</i>	+	+	+	+
<i>CSPJ015*</i>	—	+	—	—

+: Significantly deviated from Hardy-Weinberg equilibrium ( $P < 0.05$ )

Significant differences of haplotype distributions of the mtDNA marker were detected among the localities

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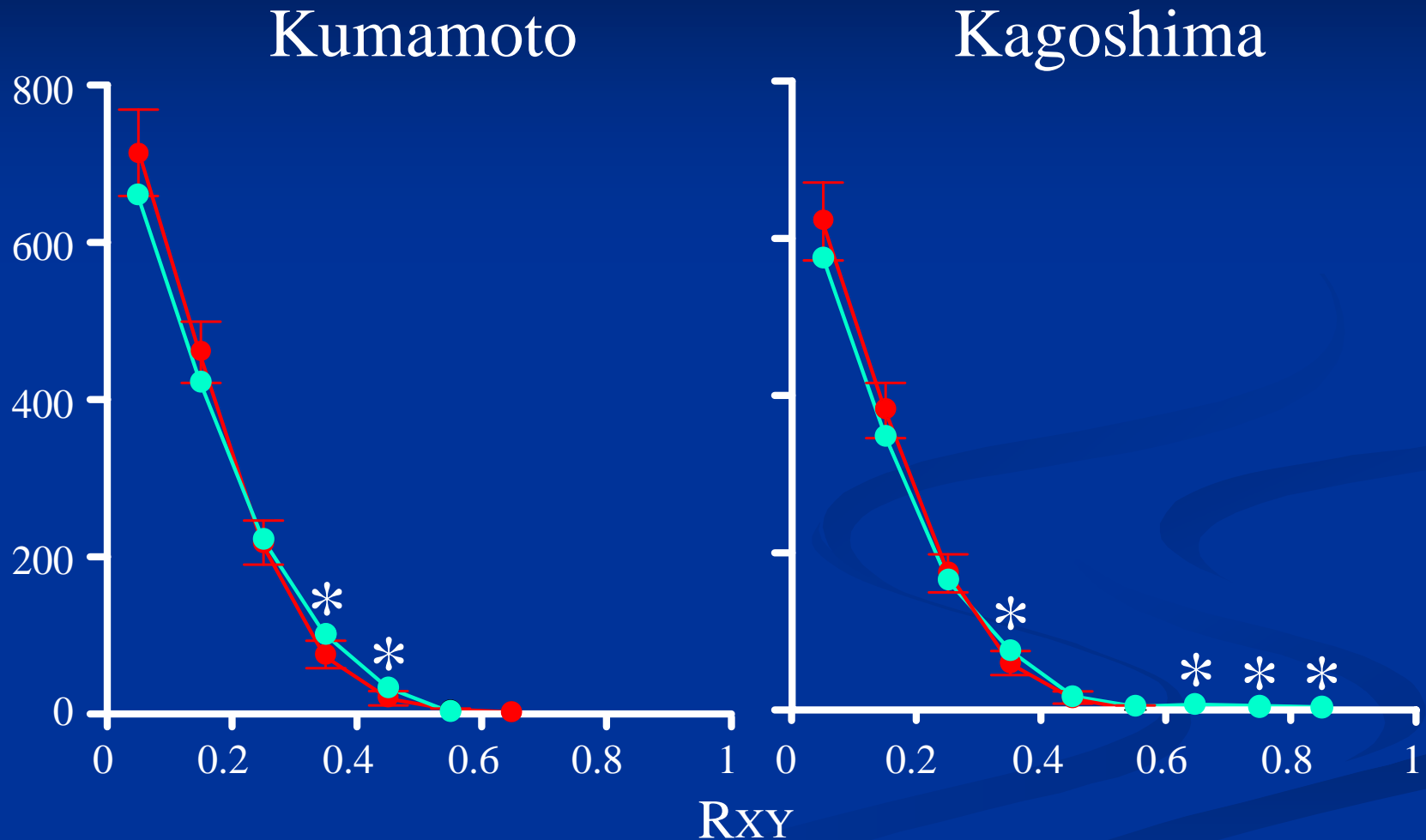
	Aichi	Ehime	Kuma- moto
Ehime	-		
Kumamoto	-	+	
Kagoshima	+	+	+

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+ : Significant ( $P < 0.05$ )



# $R_{XY}$ tended to be high in Kumamoto and Kagoshima



●:Observed value    ●:Simulated value    \*:Significant ( $P < 0.05$ )

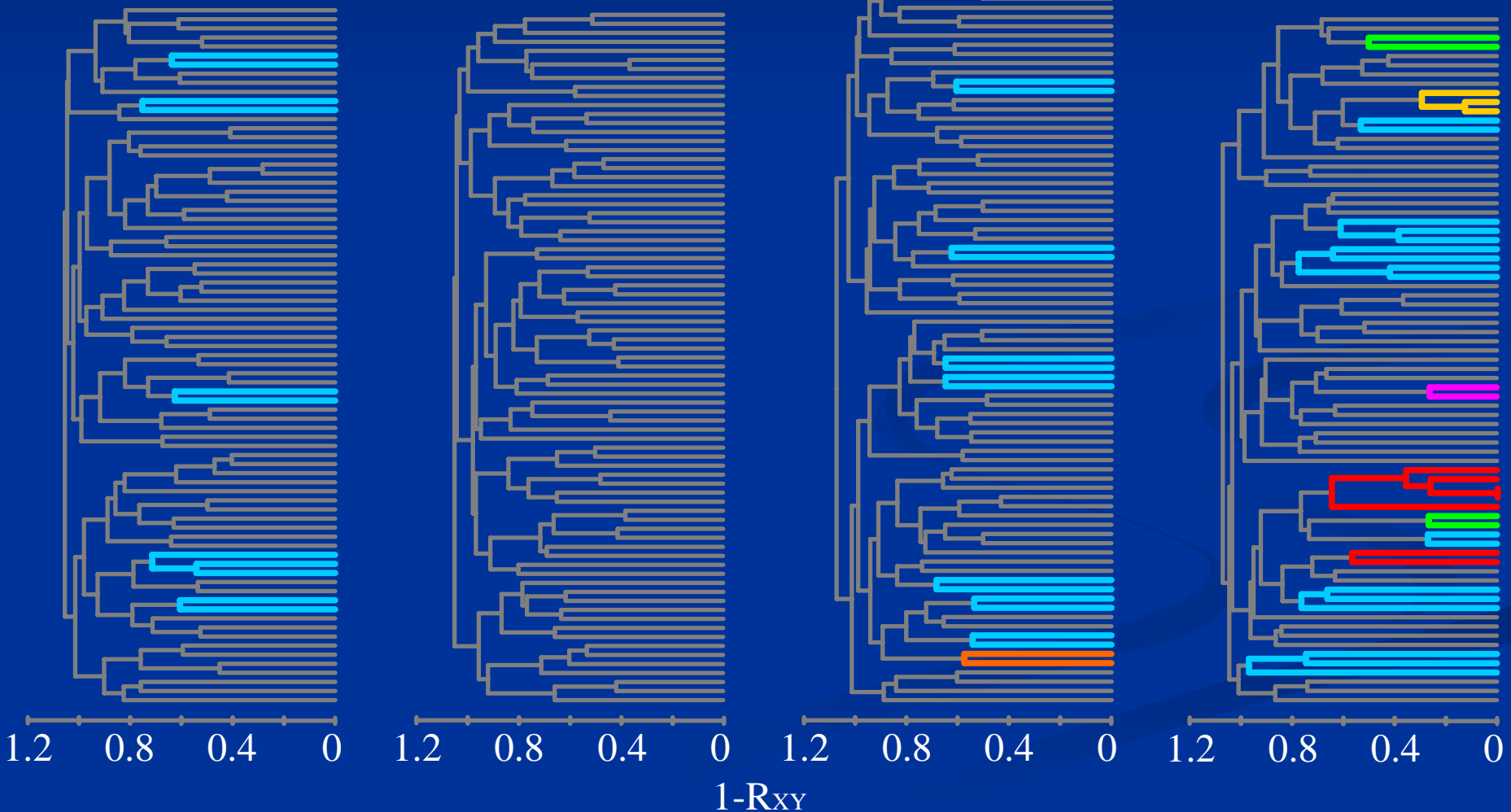
# Closely related individuals tended to share mtDNA haplotypes in Kumamoto and Kagoshima

Aichi

Ehime

Kumamoto

Kagoshima



# Conclusion

## *Genetic analyses using MS-DNA markers*

- Genetic diversity were high in all localities.
- HWE tests suggested heterogeneity within the localities.  
→ Kin groups should be existed in the localities.
- No genetic difference was detected among the localities.  
→ Gene flows among the localities are large.

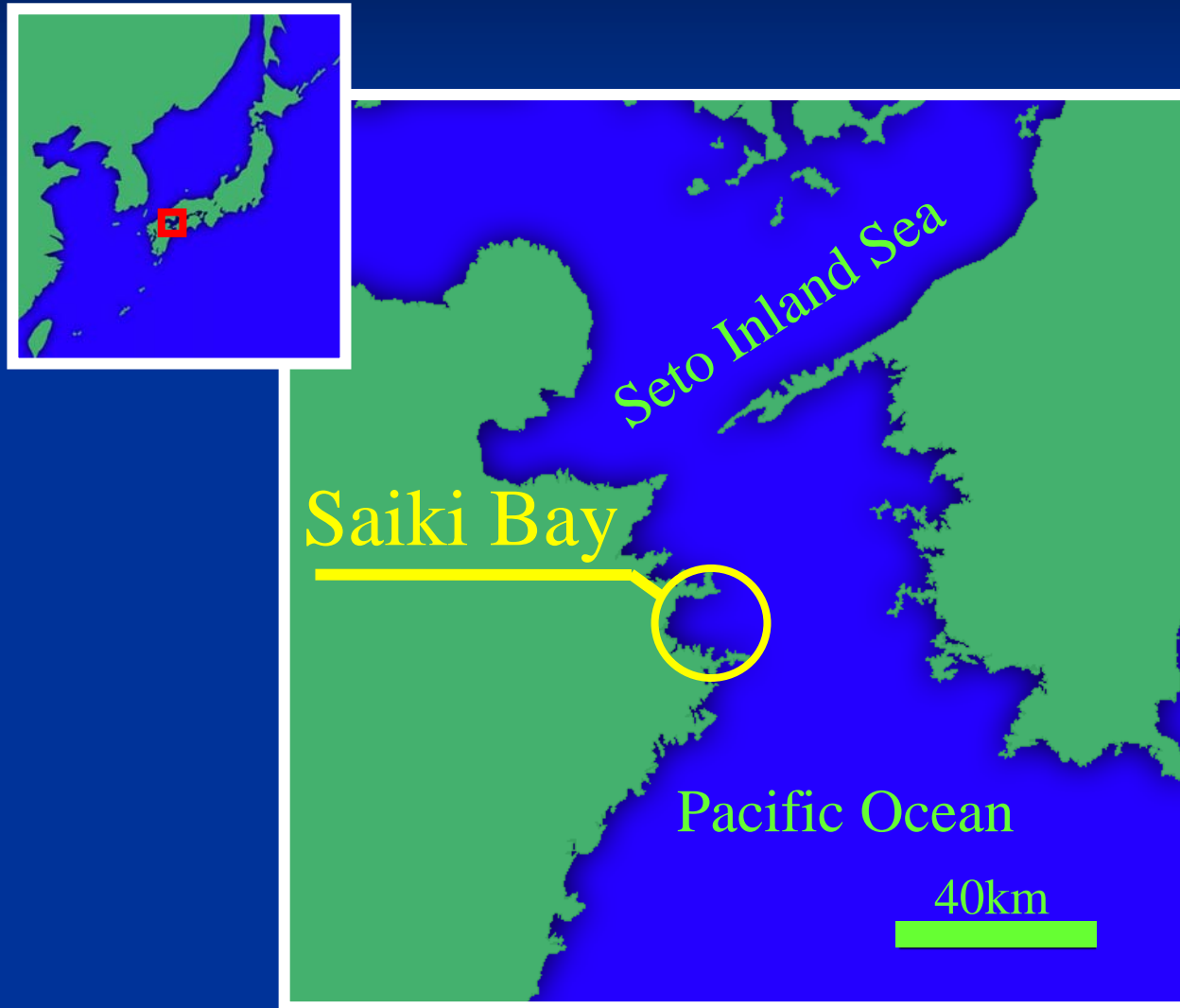
## *Genetic analyses using mtDNA markers*

- Genetic diversity were high in all localities.
- Genetic differences were significant among the localities.  
→ It is caused by the heterogeneity within the localities.

The relatedness should be useful for the detailed population genetic analysis.

*Assessment of genetic diversity  
of stocked population*

# Location of the survey area in this analysis



# Detail of the prawn stocking at Saiki Bay in 2005

No. of released prawns: 693,000

No. of marked prawns: 197,000

Size at release: 5cm in TL

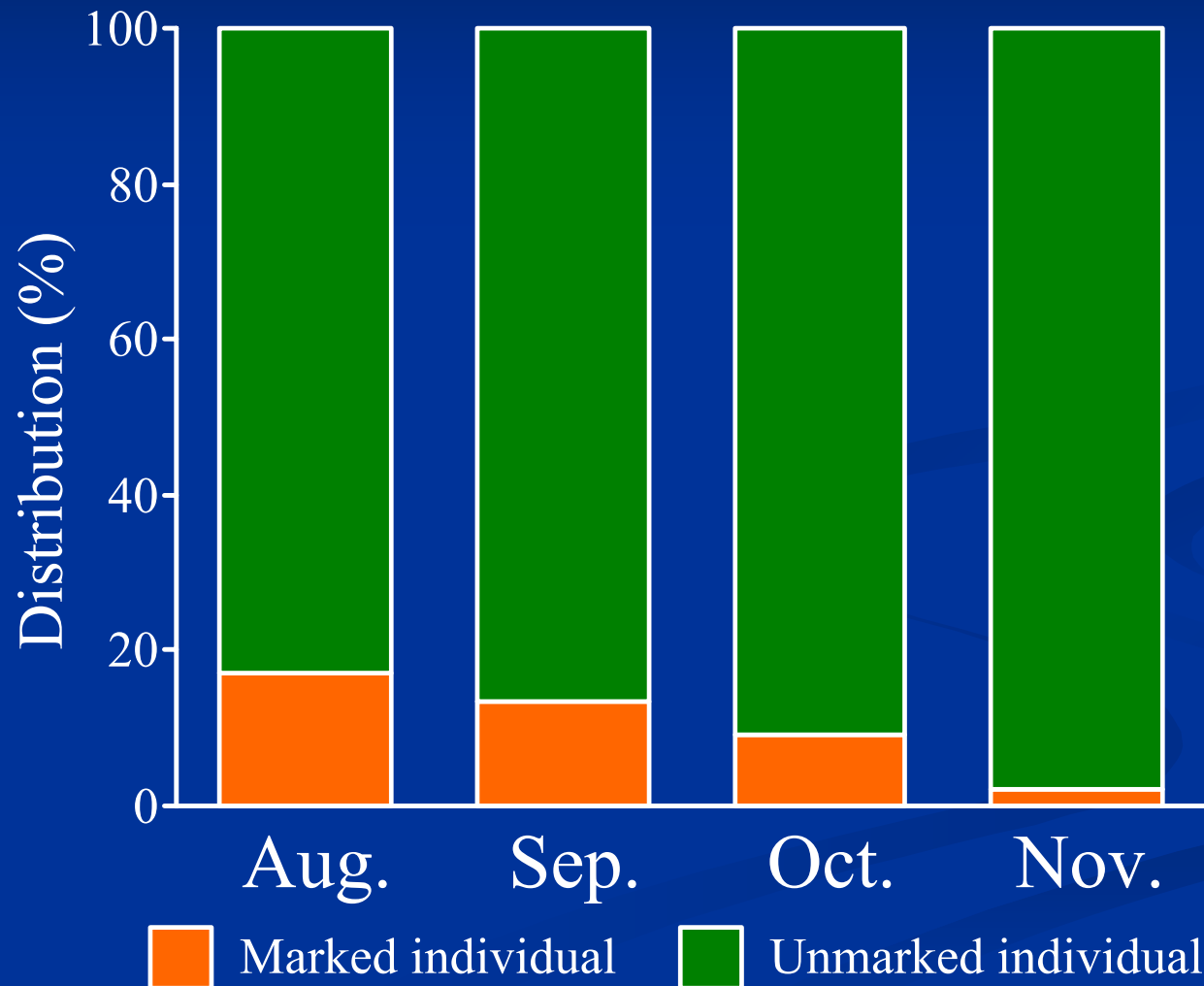
Date of release: from Jul. to Aug. '05

## *Marked prawn*

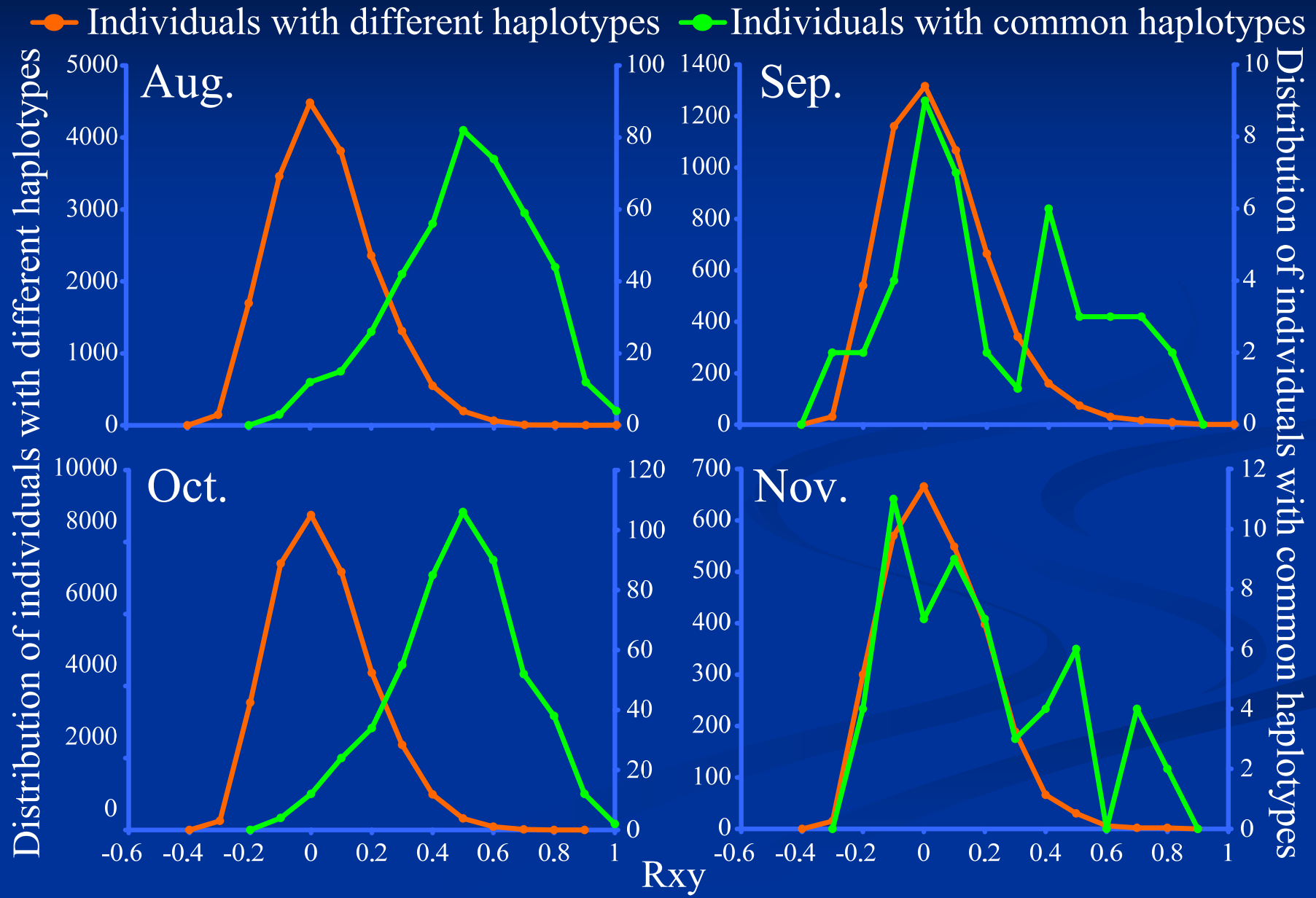
A right side of  
caudal appendage  
was cut off



# Distributions of marked individuals in the prawns caught in Saiki Bay



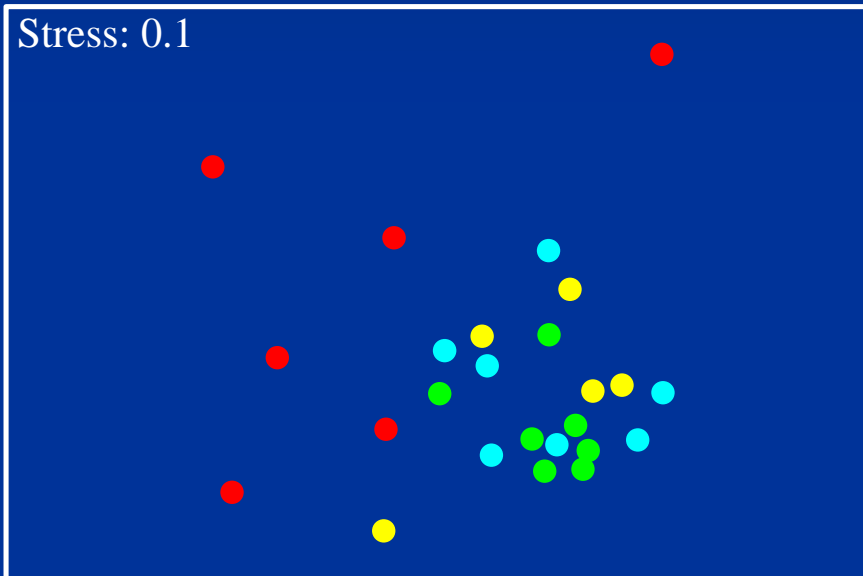
# The individuals sharing haplotypes showed relatively high relatedness



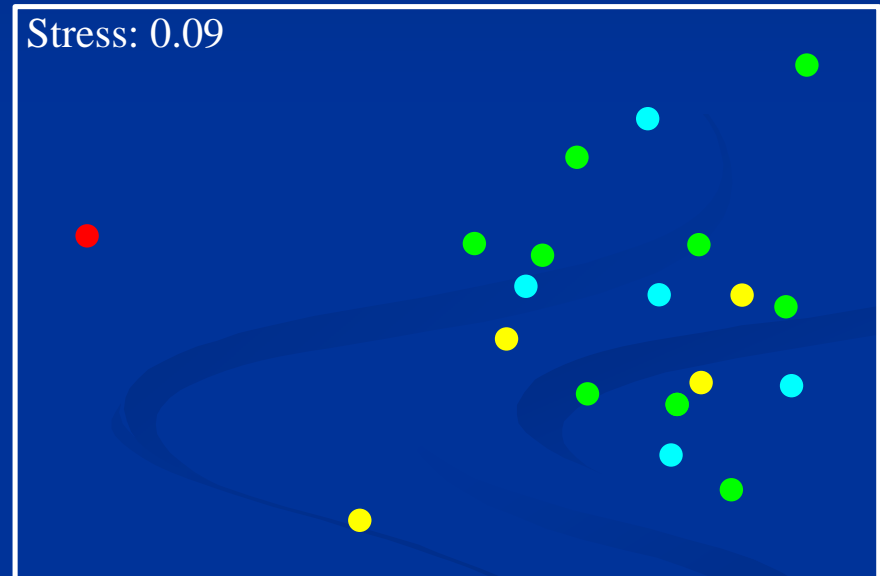


# Genetic relatedness among individuals with common haplotypes

Haplotype #3



Haplotype #30



Month of sampling

● Aug. ● Sep. ● Oct. ● Nov.

# Future directions

## *1. Assessment of genetic diversity of the wild population*

- Investigation of the degree of gene flow among localities.
- Investigation of population dynamics in each localities.

## *2. Assessment of genetic diversity of stocked population*

- Investigation of the stocking effectiveness.
- Investigation of the genetic influences of the stocking.